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RESEARCH ARTICLE

Studies of the Polymorphism of the GH Gene Affecting Economically Useful Traits of Hereford Cattle

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ABSTRACT

Modern trends in agricultural science and production are characterized by the active introduction of molecular genetic methods that make it possible to develop effective breeding strategies in animal husbandry. Studies conducted on different breeds often show contradictory results on the relationship of polymorphic gene variants with productive traits, which is explained by the complexity of the genetic regulation of traits and, possibly, the low degree of influence of individual alleles on the formation of multifactorial traits. Therefore, further research is urgently needed to accumulate information about the functioning of genes, the possibility of using polymorphism to control the genetic diversity of populations, in order to predict their productivity.

The aim of this study was to investigate the polymorphism of the GH gene, which affects the economically useful characteristics of Hereford cattle.

INTRODUCTION

Molecular genetic approaches enable analysis of protein polymorphism and DNA markers to assess genetic variability at the population level. Due to the low level of protein polymorphism and, consequently, the limited applicability of protein-based markers for diversity studies, DNA-level polymorphism is preferentially used for molecular genetic characterization.

Increasing beef production remains one of the most challenging tasks for the livestock sector in southern Russia, requiring improved efficiency in the use of available breed resources of both domestic and imported origin.

It should be noted that beef cattle bred within the Russian Federation account for only 4.0% of the total demand for meat products [1, p.21; 2, p.1920; 3, e11].

The most practical and accessible approach for early prediction of productive traits in beef cattle is genotyping for genes associated with productivity traits.

Particularly relevant are studies aimed at identifying genetic polymorphisms in genes associated with the formation of quantitative and qualitative characteristics of muscle and adipose tissues in beef cattle. The GH gene is one of the key pituitary regulators of somatic growth in animals and also plays a significant role in carbohydrate and lipid metabolism [4, p.48; 5, p.78; 6, p.3; 7, 04027].

The Hereford breed is of particular importance in Russia, as it ranks among the three most widespread breeds. Hereford cattle are characterized by their ability to produce high-quality meat with pronounced marbling and high nutritional value. In this regard, the effect of GH gene polymorphism on the productive traits of Hereford cattle requires more detailed investigation.

Therefore, the range of candidate genes directly or indirectly involved in the formation of economically important and adaptive traits should be expanded and studied across different

populations and breeds, under varying climatic, geographical, and management conditions [8, p.92; 9, p.289; 10, 012052; 11, p.1584; 12, p.386; 13, p. 161370; 14, p.113; 15 p.1; 16 p.216; 17, p.5978; 18, p.2].

The GH gene is localized on chromosome 19 in the q26 region; its length is 1800 base pairs and it consists of five exons and four introns. The gene polymorphism is caused by C→G substitution at nucleotide position 2141, resulting in an amino acid substitution from leucine to valine.

MATERIALS AND METHODS

The genetic structure of the Hereford cattle population was analyzed using animals from the agricultural cooperative "Aleksandrovsky", located in the Myasnikovsky District of the Rostov Region (Fig. 1, 47.449051, 39.368991).

Figure 1: Location of the agricultural cooperative "Aleksandrovsky"

The distance to the district center, the village of Chaltyr, is 25 km, and to the regional center, the city of Rostov-on-Don, 40 km. The natural and climatic conditions of the Myasnikovsky District are classified as moderately continental, characterized by insufficient precipitation, hot and dry summers, moderately cold winters, and short warm spring and autumn periods. The cooperative is a registered breeding farm and specializes in beef cattle production.

All animals were maintained under optimal conditions in accordance with zoohygienic and husbandry standards.

For molecular genetic analysis, blood samples were collected from experimental animals (n=100). Peripheral blood was obtained by jugular venipuncture into Vacuette vacuum tubes (9.0 mL) containing ethylenediaminetetraacetic acid (EDTA-K3) as an anticoagulant at a final concentration of 4.0 mg/mL.

Biological material was collected during routine animal evaluation (bonitation). All measures were taken to minimize animal distress and to reduce the number of experimental samples.

DNA extraction from blood samples was performed according to standard manufacturer protocols using the DNA-Extran-2 kit (Syntol LLC, Russia) and the Cleanup Mini kit for purification of DNA from reaction mixtures (Evrogen JSC, Russia). Gene polymorphism was assessed by PCR-RFLP genotyping using the following primers:

GH-F: 5′-GCT-GCT-CCT-GAG-CCT-TCG-3′
GH-R: 5′-GCG-GCG-GCA-CTT-CAT-GAC-CCT-3′

PCR conditions: initial denaturation ("hot start") at 94°C for 5 min; followed by 32 cycles of denaturation at 94°C for 60 s, annealing at 60°C for 60 s, and extension at 72°C for 60 s; final extension at 72°C for 10 min. Restriction digestion of amplification products was performed using Alu I.

Restriction fragments of the GH gene were separated by electrophoresis in 2% agarose gel (120 V) in 1×TBE buffer containing 0.5 μg/mL ethidium bromide for 30 min and visualized under UV light using a gel documentation system.

RESULTS AND DISCUSSION

Data on genotype and allele frequencies of the GH gene are presented in Figures 2 and 3.

Analysis of genotyping results showed that GH gene polymorphism in Hereford cattle is represented by two alleles, C and G.

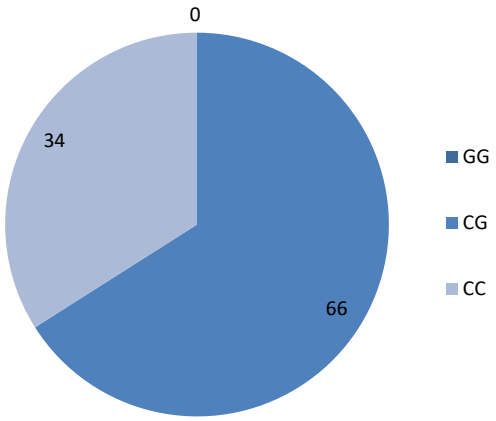

Figure 2: Frequency of GH gene genotypes

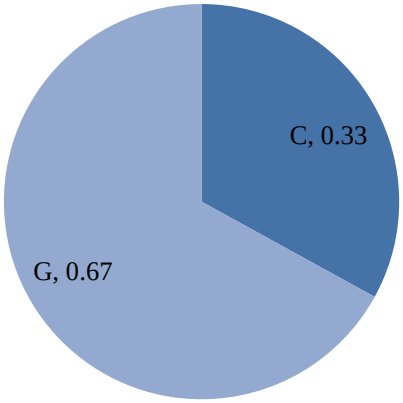

Figure 3: Frequency of GH gene alleles

The presence of two genotypes was established: GH^{cc} (66%) and GH^{cg} (34%); the G allele was predominant, with the highest frequency in the CG genotype.

Table 1 presents the results of the assessment of meat productivity in Hereford cattle depending on GH gene variants.

Table 1: Meat productivity of cattle with different GH gene genotypes

Indicators	**Genotypes**	
	GH^{CG}	GH^{CC}
Pre-slaughter live weight, kg	505,0±7,0*	475,0±6,5
Hot carcass weight, kg	294,4±4,3**	273,1±3,5
Carcass yield, %	58,29±0,19*	57,50±0,18
Internal fat weight, kg	18,6±0,8	18,1±0,4
Internal fat yield, %	3,68±0,11	3,81±0,10

According to the results of genetic analysis in the Hereford cattle population, the absence of the homozygous genotype GH^{gg} does not allow assessment of its effect on meat productivity.

However, within the studied herd, animals with the GH^{cg} genotype demonstrated superior meat traits; their carcasses were characterized by well-developed musculature and moderate fat deposition. Comparative analysis of slaughter traits among different genotypes showed that the highest pre-slaughter live weight and hot carcass weight were observed in heterozygous animals. Carcass yield in individuals with the GH^{cg} genotype was higher by 0.8% ($P > 0.95$). In terms of pre-slaughter live weight, GH^{cg} animals exceeded GH^{cc} counterparts by 30 kg ($P > 0.95$). A similar trend was observed for dressing percentage. Differences were observed in internal fat weight: animals with the GH^{cg} genotype exceeded GH^{cc} peers by 2.8%.

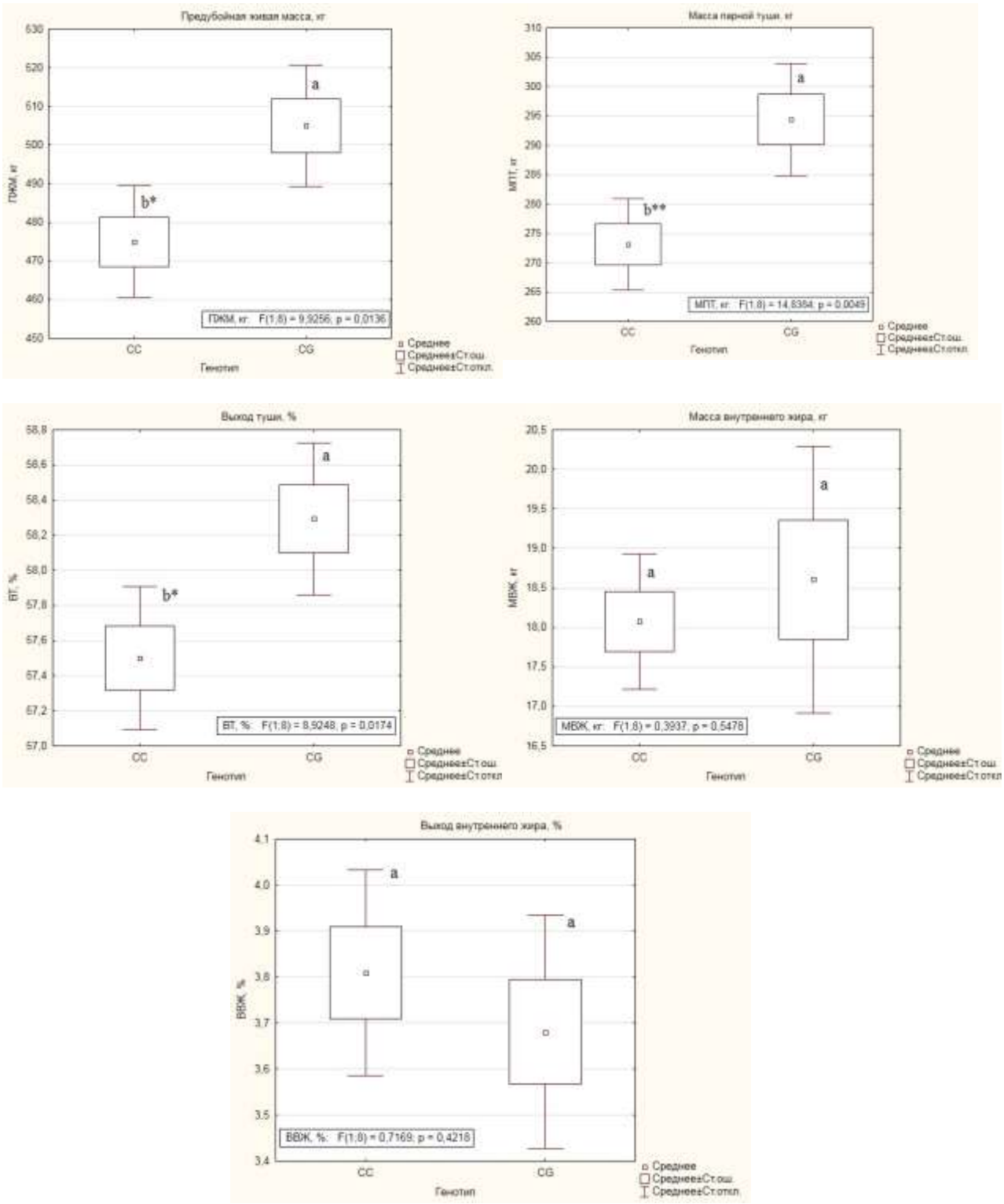

Figure 4: Differences in slaughter traits of Hereford cattle with different GH gene genotypes

Figure 4 shows differences in slaughter traits of Hereford cattle with different GH gene genotypes. A post hoc analysis was performed using Tukey's test. Thus, the obtained slaughter data indicate an effect of the growth hormone gene on the formation of meat productivity in Hereford bulls. For several traits, animals with the GH^{cg} genotype appeared preferable.

The biological and nutritional characteristics of beef products are determined by the chemical composition of the main body tissues. The principal properties of meat depend on age, sex, body

condition, and pre-slaughter status of the animals. Analysis of composite minced meat samples from bulls of different groups is presented in Table 2.

Table 2: Chemical composition of muscle tissue in bulls

Genotypes	**Content, %**			
	Moisture	Fat	Protein	Ash
GH^{CC}	76,61±0,13	1,39±0,37	21,00±0,73	0,99±0,02
GH^{CG}	76,00±0,47	1,90±0,89	21,12±0,61	0,98±0,04

Muscle tissue of animals with the GH^{cg} genotype was characterized by higher protein and fat content compared to the GH^{cc} genotype by 0.12% and 0.51%, respectively ($P < 0.01$).

CONCLUSION

1. A comparative analysis of slaughter traits in Hereford bulls of different genotypes showed that the highest pre-slaughter live weight and hot carcass weight were observed in heterozygous animals. Carcass yield in individuals with the GH^{cg} genotype was higher by 0.8% ($P > 0.95$).
2. In terms of pre-slaughter live weight, GH^{cg} animals exceeded GH^{cc} counterparts by 30 kg ($P > 0.95$). A similar trend was observed for dressing percentage.
3. Differences were identified in internal fat weight: animals with the GH^{cg} genotype exceeded GH^{cc} peers by 2.8%.
4. GH gene polymorphism affects the chemical composition of meat; muscle tissue is characterized by a higher content of intrafiber and interbundle fat inclusions.

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